

RAW SEQUENCE LISTING

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Application Serial Number: 10/825,026
Source: IFW
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IFWO

RAW SEQUENCE LISTING

DATE: 01/13/2005

PATENT APPLICATION: US/10/825,026

TIME: 11:37:16

Input Set : D:\03-03-US.ST25.txt

Output Set: N:\CRF4\01132005\J825026.raw

3 <110> APPLICANT: Aventis Pasteur, Ltd.

5 <120> TITLE OF INVENTION: Tumor Antigen BFA-5 for Prevention and/or Treatment of
Cancer

7 <130> FILE REFERENCE: API-03-03-US

C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/825,026

C--> 9 <141> CURRENT FILING DATE: 2004-04-15

9 <150> PRIOR APPLICATION NUMBER: 60/462,945

10 <151> PRIOR FILING DATE: 2004-04-15

12 <160> NUMBER OF SEQ ID NOS: 106

14 <170> SOFTWARE: PatentIn version 3.2

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 3846

18 <212> TYPE: DNA

19 <213> ORGANISM: Homo sapiens

21 <400> SEQUENCE: 1

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26	cagatgtcag	aaaatacga	tcagagtgat	gctgcagaac	taaatcataa	ggaggaacat	180
28	agcttgcatg	ttcaagatcc	atcttctagc	agtaagaagg	acttgaaaag	cgcagttctg	240
30	agtgagaagg	ctggcttcaa	ttatgaaagc	cccagtaagg	gaggaaaactt	tccctccttt	300
32	ccgcattgat	aggtgacaga	cagaaatatg	ttggctttct	catttccagc	tgctggggga	360
34	gtctgtgagc	ccttgaagtc	tccgcaaaga	gcagaggcag	atgaccctca	agatatggcc	420
36	tgcacccctc	caggggactc	actggagaca	aaggaagatc	agaagatgtc	accaaaggct	480
38	acagaggaaa	cagggcaagc	acagagtggg	caagccaatt	gtcaagggtt	gagcccagtt	540
40	tcagtggcct	caaaaaaccc	acaagtgcct	tcagatgggg	gtgtaagact	gaataaatcc	600
42	aaaactgact	tactgggtgaa	tgacaaccca	gaccgggcac	ctctgtctcc	agagcttcag	660
44	gacttttaaat	gcaatatctg	tggatatggg	tactacggca	acgacccac	agatctgatt	720
46	aagcacttcc	gaaagtatca	cttaggactg	cataaccgca	ccaggcaaga	tgctgagctg	780
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54	cggaaaacac	cagattgccca	agggaaacac	aagtatttcc	gctgtaaatt	ctgcaatttc	1020
56	acttatatgg	gcaactcatc	caccgaatta	gaacaacatt	ttcttcagac	tcacccaaac	1080
58	aaaataaaaag	cttctctccc	ctcctctgag	gttgcaaaac	cttcagagaa	aaactctaac	1140
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62	ataacagtca	aagcaggaga	tgacactcct	gttgggtact	cagtgcccat	aaagcccctc	1260
64	gattcctcta	gacaaaatgg	tacagaggcc	accagttaact	actggtgtaa	atcttgtagt	1320
66	ttcagctgtg	agtcactctag	ctcacttaaa	ctgtagaac	attatggcaa	gcagcacgga	1380
68	gcagtgcagt	caggcggcct	taatccagag	ttaaatgata	agctttccag	gggctctgtc	1440
70	attaatcaga	atgatctagc	caaaagttca	gaaggagaga	caatgaccaa	gacagacaag	1500
72	agctcgagtg	gggctaaaaa	gaaggacttc	tccagcaagg	gagccgagga	taatattgga	1560
74	acgagctata	attgtcagtt	ctgtgacttc	cgatattcca	aaagccatgg	ccctgatgta	1620
76	attgtagtgg	ggccacttct	ccgtcattat	caacagctcc	ataacattca	caagtgtacc	1680
78	attaaacact	gtccattctg	tcccagagga	ctttgcagcc	cagaaaagca	ccttggagaa	1740

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80 attacttattc cgtttgcttg tagaaaaagt aattgttccc actgtgcact cttgcttctg 1800
82 cacttgctctc ctggggcggc tgaagctcg cgagtcaaac atcagtgcc tcaagtgttca 1860
84 ttcaccaccc ctgacgtaga tgtactcctc tttcactatg aaagtgtgca tgagtcccaa 1920
86 gcatcggtatg tcaaacaaga agcaaatcac ctgcaaggat cggatgggca gcagtctgtc 1980
88 aaggaaagca aagaacactc atgtaccaa tgtgatttta ttacccaagt ggaagaagag 2040
90 atttcccgac actacaggag agcacacagc tgctacaaat gccgtcagt cagttttaca 2100
92 gctgccgata ctgagtcact actggagcac ttcaacactg ttacttgcca ggaacaggac 2160
94 atcactacag ccaacggcga agaggacggg catgccatat ccaccatcaa agaggagccc 2220
96 aaaattgact tcagggtcta caatctgcta actccagact ctaaaatggg agagccagtt 2280
98 tctgagagtg tgggtgaagag agagaagctg gaagagaagg acgggctcaa agagaaagtt 2340
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102 cgggggagtc cgtcatcac ccaagcaagc ctggggctgc tgacgcctgt gtctggcacc 2460
104 caagagcaga caaagactct aagggatagt cccaatgtgg aggccgcca tctggcgca 2520
106 cctatttatg gcttggctgt ggaaaccaag ggattcctgc agggggcgcc agctggcgga 2580
108 gagaagtctg gggccctccc ccagcagtat cctgcatcgg gagaaaacaa gtccaaggat 2640
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114 ggcctctacc agaagcttca ctgactccc aggcctttaa acatcattaa acaaaacaac 2820
116 ggtgagcaga ttattaggag gagaacaaga aagcgcctta acccagaggc acttcaggct 2880
118 gagcagctca acaaacagca gaggggcagc aatgaggagc aagtcaatgg aagcccgtta 2940
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128 agttctgaga gaggcagtcc tatagaaaag tacatgagac ctgcgaaaca cccaaattat 3240
130 tcaccaccag gcagccctat tgaaaagtac cagtaccac tttttggact tccctttgta 3300
132 cataatgact tccagagtga agctgattgg ctgcggttct ggagtaaata taagctctcc 3360
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136 tatgtgcctt atcccacctt caatctgcct cctcattttt cagctgttgg atcagacaat 3480
138 gacattcctc tagatttggc gatcaagcat tccagacctg ggccaactgc aaacggtgcc 3540
140 tccaaggaga aaacgaaggc accaccaa atgtaaaaatg aaggtccctt gaatgtagta 3600
142 aaaacagaga aagttgatag aagtactcaa gatgaacttt caacaaaatg tgtgcactgt 3660
144 ggcattgtct ttctggatga agtgatgtat gctttgcata tgagttgcca tgggtgacagt 3720
146 ggacctttcc agtgcagcat atgccagcat ctttgcacgg acaaatatga cttcacaaca 3780
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153 <210> SEQ ID NO: 2

154 <211> LENGTH: 1281

155 <212> TYPE: PRT

156 <213> ORGANISM: Homo sapiens

158 <400> SEQUENCE: 2

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161 1 5 10 15
164 Glu Gly Gln Ile Leu Glu Pro Ile Gly Thr Glu Ser Lys Val Ser Gly
165 20 25 30
168 Lys Asn Lys Glu Phe Ser Ala Asp Gln Met Ser Glu Asn Thr Asp Gln
169 35 40 45
172 Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val
173 50 55 60

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176 Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
177 65              70              75              80
180 Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn
181              85              90              95
184 Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala
185              100             105             110
188 Phe Ser Phe Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro
189              115             120             125
192 Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser
193              130             135             140
196 Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
197 145              150             155             160
200 Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly
201              165              170             175
204 Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp
205              180             185             190
208 Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp
209              195             200             205
212 Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys
213              210             215             220
216 Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile
217 225              230             235             240
220 Lys His Phe Arg Lys Tyr His Leu Gly Leu His Asn Arg Thr Arg Gln
221              245             250             255
224 Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln
225              260             265             270
228 Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser
229              275             280             285
232 Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly
233              290             295             300
236 Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly
237 305              310             315             320
240 Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
241              325             330             335
244 Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln
245              340             345             350
248 His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
249              355             360             365
252 Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro
253              370             375             380
256 Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys
257 385              390             395             400
260 Ile Thr Val Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro
261              405             410             415
264 Ile Lys Pro Leu Asp Ser Ser Arg Gln Asn Gly Thr Glu Ala Thr Ser
265              420             425             430
268 Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser
269              435             440             445
272 Leu Lys Leu Leu Glu His Tyr Gly Lys Gln His Gly Ala Val Gln Ser

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273      450      455      460
276 Gly Gly Leu Asn Pro Glu Leu Asn Asp Lys Leu Ser Arg Gly Ser Val
277 465      470      475      480
280 Ile Asn Gln Asn Asp Leu Ala Lys Ser Ser Glu Gly Glu Thr Met Thr
281      485      490      495
284 Lys Thr Asp Lys Ser Ser Ser Gly Ala Lys Lys Lys Asp Phe Ser Ser
285      500      505      510
288 Lys Gly Ala Glu Asp Asn Met Val Thr Ser Tyr Asn Cys Gln Phe Cys
289      515      520      525
292 Asp Phe Arg Tyr Ser Lys Ser His Gly Pro Asp Val Ile Val Val Gly
293      530      535      540
296 Pro Leu Leu Arg His Tyr Gln Gln Leu His Asn Ile His Lys Cys Thr
297 545      550      555      560
300 Ile Lys His Cys Pro Phe Cys Pro Arg Gly Leu Cys Ser Pro Glu Lys
301      565      570      575
304 His Leu Gly Glu Ile Thr Tyr Pro Phe Ala Cys Arg Lys Ser Asn Cys
305      580      585      590
308 Ser His Cys Ala Leu Leu Leu Leu His Leu Ser Pro Gly Ala Ala Gly
309      595      600      605
312 Ser Ser Arg Val Lys His Gln Cys His Gln Cys Ser Phe Thr Thr Pro
313      610      615      620
316 Asp Val Asp Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln
317 625      630      635      640
320 Ala Ser Asp Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly
321      645      650      655
324 Gln Gln Ser Val Lys Glu Ser Lys Glu His Ser Cys Thr Lys Cys Asp
325      660      665      670
328 Phe Ile Thr Gln Val Glu Glu Glu Ile Ser Arg His Tyr Arg Arg Ala
329      675      680      685
332 His Ser Cys Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr
333      690      695      700
336 Gln Ser Leu Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp
337 705      710      715      720
340 Ile Thr Thr Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile
341      725      730      735
344 Lys Glu Glu Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro
345      740      745      750
348 Asp Ser Lys Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu
349      755      760      765
352 Lys Leu Glu Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser
353      770      775      780
356 Ser Ser Asp Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu
357 785      790      795      800
360 Arg Gly Ser Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro
361      805      810      815
364 Val Ser Gly Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn
365      820      825      830
368 Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu
369      835      840      845

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372 Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly
373      850                      855                      860
376 Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp
377 865                      870                      875                      880
380 Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys
381                      885                      890                      895
384 Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn
385                      900                      905                      910
388 Gly Gly Tyr Val Cys Asn Ala Cys Gly Leu Tyr Gln Lys Leu His Ser
389                      915                      920                      925
392 Thr Pro Arg Pro Leu Asn Ile Lys Gln Asn Asn Gly Glu Gln Ile
393      930                      935                      940
396 Ile Arg Arg Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala
397 945                      950                      955                      960
400 Glu Gln Leu Asn Lys Gln Gln Arg Gly Ser Asn Glu Glu Gln Val Asn
401                      965                      970                      975
404 Gly Ser Pro Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His
405                      980                      985                      990
408 Gln Arg Glu Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly
409      995                      1000                      1005
412 Ser Leu Thr Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser
413      1010                      1015                      1020
416 Gln Thr Leu Asp Ile His Lys Arg Met Gln Pro Leu His Ile Gln
417      1025                      1030                      1035
420 Ile Lys Ser Pro Gln Glu Ser Thr Gly Asp Pro Gly Asn Ser Ser
421      1040                      1045                      1050
424 Ser Val Ser Glu Gly Lys Gly Ser Ser Glu Arg Gly Ser Pro Ile
425      1055                      1060                      1065
428 Glu Lys Tyr Met Arg Pro Ala Lys His Pro Asn Tyr Ser Pro Pro
429      1070                      1075                      1080
432 Gly Ser Pro Ile Glu Lys Tyr Gln Tyr Pro Leu Phe Gly Leu Pro
433      1085                      1090                      1095
436 Phe Val His Asn Asp Phe Gln Ser Glu Ala Asp Trp Leu Arg Phe
437      1100                      1105                      1110
440 Trp Ser Lys Tyr Lys Leu Ser Val Pro Gly Asn Pro His Tyr Leu
441      1115                      1120                      1125
444 Ser His Val Pro Gly Leu Pro Asn Pro Cys Gln Asn Tyr Val Pro
445      1130                      1135                      1140
448 Tyr Pro Thr Phe Asn Leu Pro Pro His Phe Ser Ala Val Gly Ser
449      1145                      1150                      1155
452 Asp Asn Asp Ile Pro Leu Asp Leu Ala Ile Lys His Ser Arg Pro
453      1160                      1165                      1170
456 Gly Pro Thr Ala Asn Gly Ala Ser Lys Glu Lys Thr Lys Ala Pro
457      1175                      1180                      1185
460 Pro Asn Val Lys Asn Glu Gly Pro Leu Asn Val Val Lys Thr Glu
461      1190                      1195                      1200
464 Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys Cys Val
465      1205                      1210                      1215
468 His Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu His

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date